

SequenceListingSecondSubstitute679872.txt
SEQUENCE LISTING

<110> Desire, Laurent

<120> BACE455, AN ALTERNATIVE SPLICE VARIANT OF THE HUMAN
BETA-SECRETASE

<130> 67987.000002

<140> 10/578,493

<141> 2006-05-05

<150> PCT/IB2004/003897

<151> 2004-11-05

<150> 60/517,401

<151> 2003-11-03

<160> 36

<170> PatentIn version 3.5

<210> 1

<211> 1368

<212> DNA

<213> Homo sapiens

<400> 1		
atggcccaag	ccctgccctg	60
ggcaccacgc	acggcatccg	120
ctgcggtctg	cccgggagag	180
gtggagatgg	tggacaacct	240
gtgggcagcc	ccccgcagac	300
gtgggtgctg	ccccccacc	360
taccgggacc	tccggaagg	420
ctgggcaccg	acctggtaag	480
gctgccatca	ctgaatcaga	540
gggctggcct	atgctgagat	600
ggcagctctt	ggtatacacc	660
gtggagatca	atggacagga	720
attgtggaca	gtggcaccac	780
aaatccatca	aggcagcctc	840
cagctggtgt	gctggcaagc	900
tacctaatgg	gtgaggttac	960
ctgcggccag	tggaaagtgt	1020
cagtcaccca	cgggcactgt	1080

SequenceListingSecondSubstitute679872.txt

gatcggggccc gaaaacgaat tggctttgct gtcagcgctt gccatgtgca cgatgagttc	1140
aggacggcag cgggtgaagg cccctttgtc accttggaca tggaagactg tggctacaac	1200
attccacaga cagatgagtc aaccctcatg accatagcct atgtcatggc tgccatctgc	1260
gccctcttca tgctgccact ctgacctcatg gtgtgtcagt ggcgtgcct ccgctgcctg	1320
cgccagcagc atgatgactt tgctgatgac atctccctgc tgaagtga	1368

<210> 2
 <211> 455
 <212> PRT
 <213> Homo sapiens
 <400> 2

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Ile Ile Gly
 180 185 190

Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
 195 200 205

Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
 210 215 220

Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
 225 230 235 240

Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
 245 250 255

Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
 260 265 270

Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
 275 280 285

Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
 290 295 300

Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
 305 310 315 320

Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
 325 330 335

Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
 340 345 350

Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
 355 360 365

Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
 370 375 380

Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
 385 390 395 400

Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met
 405 410 415

Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys
 420 425 430

SequenceListingSecondSubstitute679872.txt

Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala
435 440 445

Asp Asp Ile Ser Leu Leu Lys
450 455

<210> 3
<211> 6
<212> PRT
<213> artificial

<220>
<223> distinctive fragment

<400> 3

Ile Ala Arg Ile Ile Gly
1 5

<210> 4
<211> 7
<212> PRT
<213> artificial

<220>
<223> distinctive fragment

<400> 4

Glu Ile Ala Arg Ile Ile Gly
1 5

<210> 5
<211> 8
<212> PRT
<213> artificial

<220>
<223> distinctive fragment

<400> 5

Glu Ile Ala Arg Ile Ile Gly Gly
1 5

<210> 6
<211> 8
<212> PRT
<213> artificial

<220>
<223> distinctive fragment

<400> 6

Ala Glu Ile Ala Arg Ile Ile Gly
1 5

<210> 7
 <211> 9
 <212> PRT
 <213> artificial

<220>
 <223> AEIARIIGG

<400> 7

Ala Glu Ile Ala Arg Ile Ile Gly Gly
 1 5

<210> 8
 <211> 10
 <212> PRT
 <213> artificial

<220>
 <223> distinctive fragment

<400> 8

Ala Glu Ile Ala Arg Ile Ile Gly Gly Ile
 1 5 10

<210> 9
 <211> 9
 <212> PRT
 <213> artificial

<220>
 <223> distinctive fragment

<400> 9

Tyr Ala Glu Ile Ala Arg Ile Ile Gly
 1 5

<210> 10
 <211> 10
 <212> PRT
 <213> artificial

<220>
 <223> distinctive fragment

<400> 10

Tyr Ala Glu Ile Ala Arg Ile Ile Gly Gly
 1 5 10

<210> 11
 <211> 11
 <212> PRT
 <213> artificial

```

<220>
<223> distinctive fragment

<400> 11
Tyr Ala Glu Ile Ala Arg Ile Ile Gly Gly Ile
1      5      10

<210> 12
<211> 18
<212> DNA
<213> artificial

<220>
<223> probe

<400> 12
attgccagga tcattgga                                18

<210> 13
<211> 10
<212> DNA
<213> artificial

<220>
<223> primer

<400> 13
aggcatcctg                                10

<210> 14
<211> 10
<212> DNA
<213> artificial

<220>
<223> primer

<400> 14
gggctggcct                                10

<210> 15
<211> 10
<212> DNA
<213> artificial

<220>
<223> primer

<400> 15
atgctgagat                                10

<210> 16
<211> 6
<212> DNA
<213> artificial

<220>

```

SequenceListingSecondSubstitute679872.txt

<223>	primer	
<400>	16	
tgccag		6
<210>	17	
<211>	6	
<212>	DNA	
<213>	artificial	
<220>		
<223>	primer	
<400>	17	
gatcat		6
<210>	18	
<211>	10	
<212>	DNA	
<213>	artificial	
<220>		
<223>	primer	
<400>	18	
tggaggtatc		10
<210>	19	
<211>	10	
<212>	DNA	
<213>	artificial	
<220>		
<223>	primer	
<400>	19	
gaccactcgc		10
<210>	20	
<211>	10	
<212>	DNA	
<213>	artificial	
<220>		
<223>	primer	
<400>	20	
tgtacacagg		10
<210>	21	
<211>	10	
<212>	DNA	
<213>	artificial	
<220>		
<223>	primer	
<400>	21	

SequenceListingSecondSubstitute679872.txt		
cagtcctctgg		10
<210> 22		
<211> 6		
<212> DNA		
<213> artificial		
<220>		
<223> primer		
<400> 22		
caggat		6
<210> 23		
<211> 8		
<212> DNA		
<213> artificial		
<220>		
<223> primer		
<400> 23		
ccaggatc		8
<210> 24		
<211> 10		
<212> DNA		
<213> artificial		
<220>		
<223> primer		
<400> 24		
gccaggatca		10
<210> 25		
<211> 18		
<212> DNA		
<213> artificial		
<220>		
<223> primer		
<400> 25		
attgccagga tcattgga		18
<210> 26		
<211> 21		
<212> DNA		
<213> artificial		
<220>		
<223> primer		
<400> 26		
tgactgggaa caccataa c		21


```

<210> 27
<211> 19
<212> DNA
<213> artificial

<220>
<223> primer

<400> 27
agttgtgcat gggagcgag                                19

<210> 28
<211> 19
<212> DNA
<213> artificial

<220>
<223> primer

<400> 28
cccgcagacg ctcaacatc                                19

<210> 29
<211> 21
<212> DNA
<213> artificial

<220>
<223> primer

<400> 29
cagcgagtgg tcgatactc c                                21

<210> 30
<211> 24
<212> DNA
<213> artificial

<220>
<223> primer

<400> 30
gcggatccac catggcccaa gccc                            24

<210> 31
<211> 33
<212> DNA
<213> artificial

<220>
<223> primer

<400> 31
ggggaattca cttcagcagg gagatgtcat cag                33

<210> 32
<211> 10
<212> PRT

```

<213> artificial

<220>

<223> fluorogenic App-based peptide MCA

<400> 32

Ser Glu Val Asn Leu Asp Ala Glu Phe Lys
1 5 10

<210> 33

<211> 9

<212> PRT

<213> artificial

<220>

<223> BACE inhibitor III

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa is statine

<400> 33

His Glu Val Asn Xaa Val Ala Glu Phe
1 5

<210> 34

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> beta-secretase cleavage site in APP

<400> 34

Glu Val Lys Met Asp Ala Glu
1 5

<210> 35

<211> 8

<212> PRT

<213> Homo sapiens

<400> 35

Leu Val Asn Met Ala Glu Gly Asp
1 5

<210> 36

<211> 501

<212> PRT

<213> Homo sapiens

<400> 36

SequenceListingSecondSubstitute679872.txt

Met Ala Gln Ala Leu Pro Trp Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Cys Ala Gly Phe Pro Leu Asn Gln
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
245 250 255

SequenceListingSecondSubstitute679872.txt

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
435 440 445

Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
450 455 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
465 470 475 480

Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
485 490 495

Ile Ser Leu Leu Lys
500